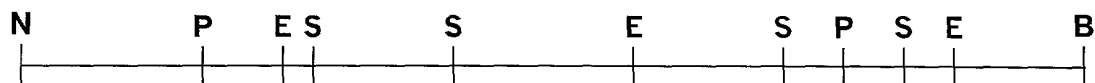


Figure 1: Restriction pattern of the HAL coding region cut with selected enzymes.

HAL



N - NdeI site introduced at the N-terminus

B - BamHI site introduced at the C-terminus

E - EagI

P - PstI

S - SphI

Figure 2: Experimentally derived peptide sequences of HAL

N-terminal

(M)ASAPQITLGLSGATAD

Internal

(M)ALADLDELLDEA

(M)GEPVEREVLRA

SEQUENCE

Figure 3: SphI digestion pattern of HAL gene showing oligonucleotide and subclones.

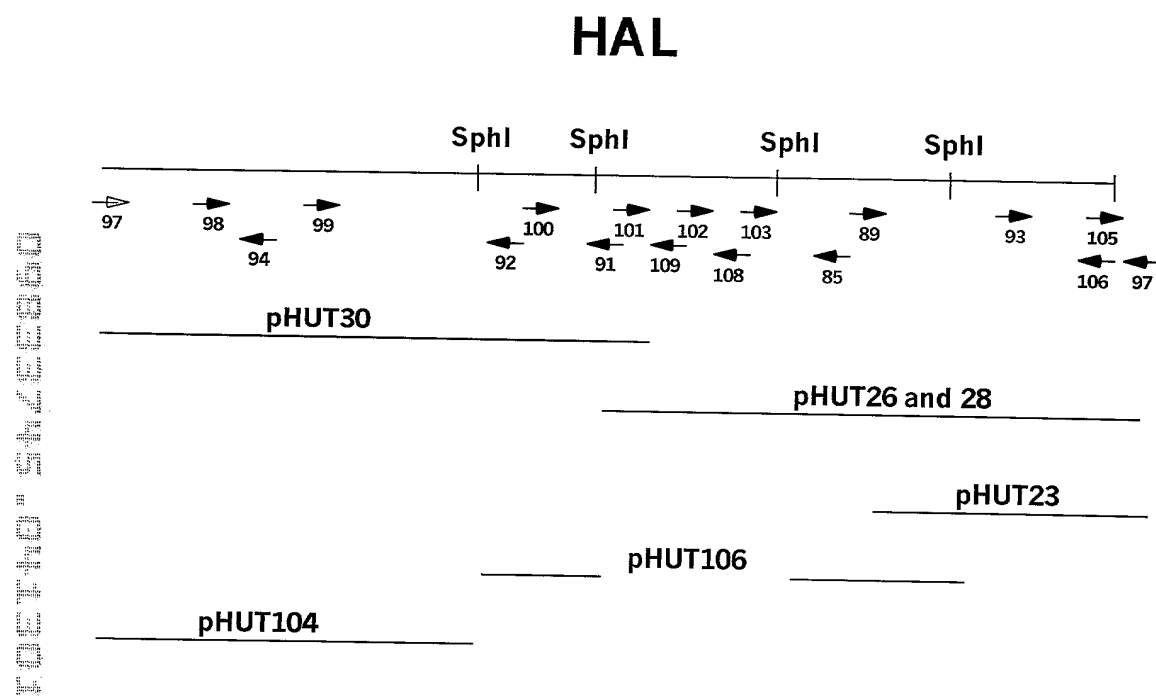


Figure 4: Histidine ammonia lyase overexpressing plasmid.

pHUT102

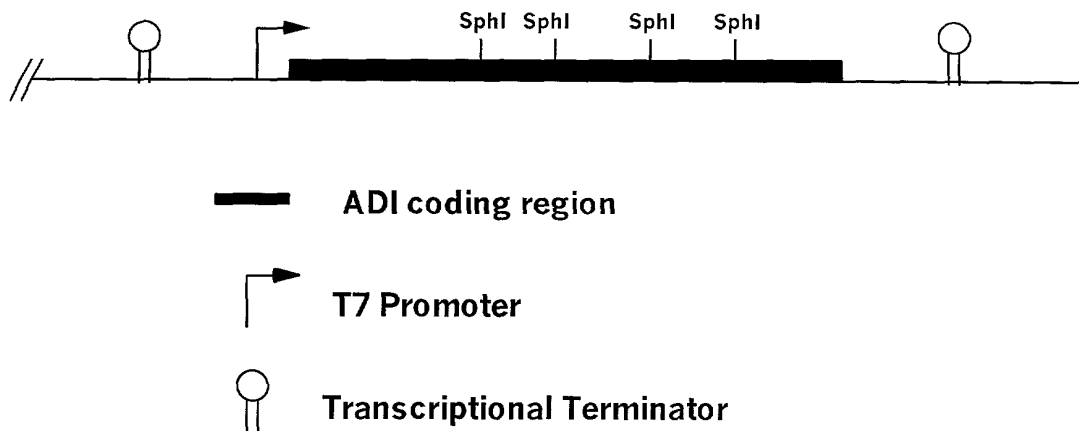


Figure 5: SDS-PAGE showing expression of HAL in *E. coli*.

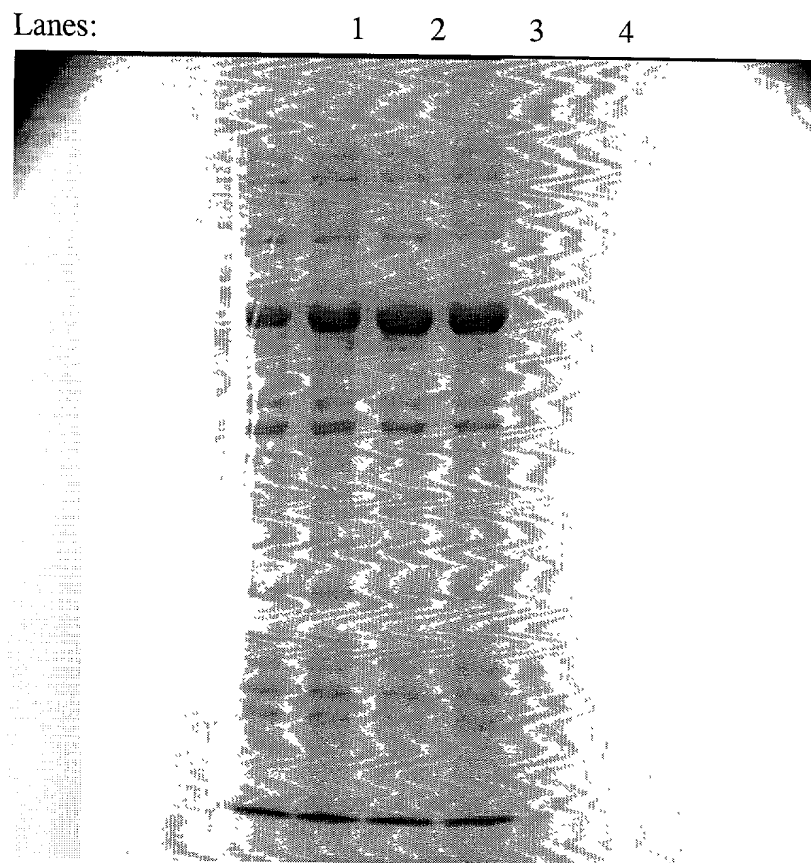


Figure 6: SDS-PAGE showing purification of HAL from *E. coli*

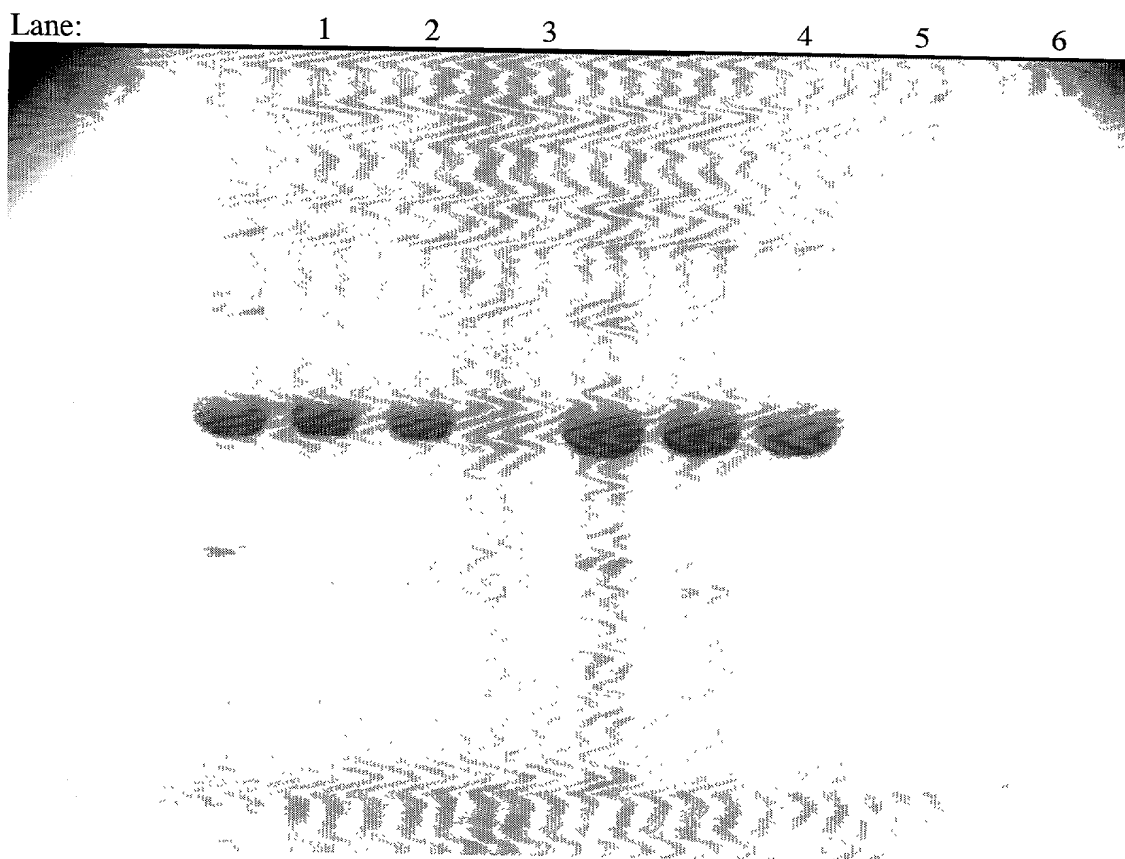
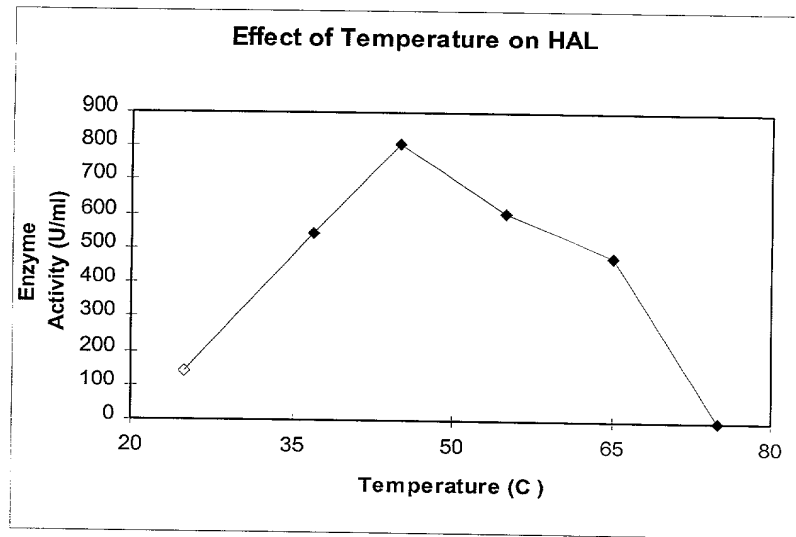


Figure 7: Effect of Temperature on HAL

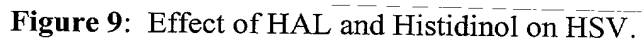


Patent 6,666,666

Figure 8: Effect of pH on HAL.



04/27/2004



A 3D bar chart showing the values of PF (Performance Factor) for six categories. The y-axis is logarithmic, ranging from 1.00E+00 to 1.00E+09. The x-axis categories are 1 through 6. The PF values decrease from category 1 to 6.

Category	PF Value
1	~1.00E+08.5
2	~1.00E+08.2
3	~1.00E+08.0
4	~1.00E+07.8
5	~1.00E+06.5
6	~1.00E+05.5

Figure 11: Effect of HAL and Histidinol on RSV.

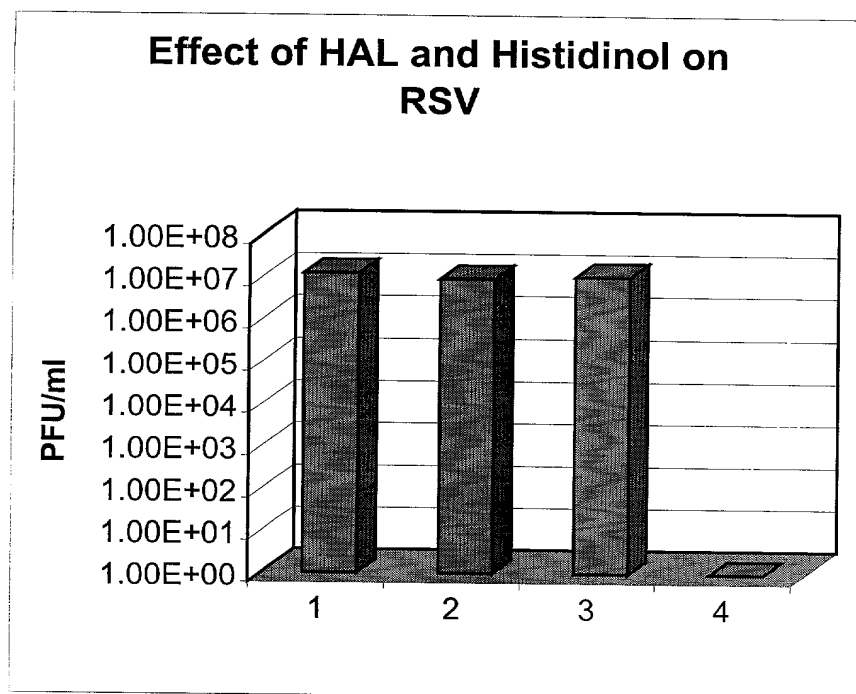
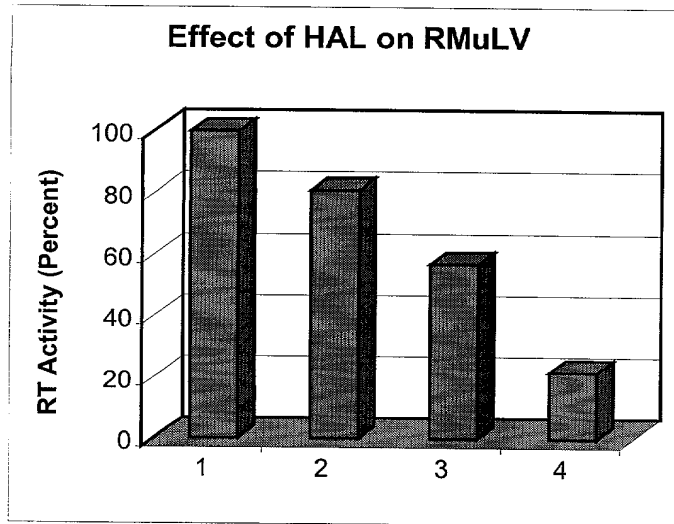


Figure 12: Effect of HAL on RMuLV.



078728/0106

Figure 13: Histidine ammonia lyase peptide sequence pileup

```

HUTH_PSEPU  -----
-
HUTH_RHIME  -----
-
HUTH_MOUSE  -----
MPRYTVHVRGEWLAVPCQDGKLTVGWLGREAVRRYMKNKPDNGGFTSVDEVQFLVHRCKG
HUTH_RAT     -----
MPRYTVHVRGEWLAVPCQDGKLSVGWLGREAVRRYMKNKPDNGGFTSVDEVRFVLRCKG
HUTH_HUMAN   -----
MPRYTVHVRGEWLAVPCQDAQLTVGWLGREAVRRYIKNKPDNGGFTSVDDAHFLVRRCKG
HUTH_CAEL    -MRLQVQIGTECVVVPCKP-DDTIHAVAKKSVEKLRRLRPK----
LPLADDYFEVVRTVG
HUTH_BACS    -----
-
HUTH_STRGR   -----
-
HUTH_CORY    -----
-

HUTH_PSEPU  -----
-
HUTH_RHIME  -----
-
HUTH_MOUSE  LGLLDNEDELEVALEDNEFVEVVIEGDVMS-----PDFIPSQPEGVFLYSKYR---
-
HUTH_RAT     LGLLDNEDLLEVALEDNEFVEVVIEGDVMS-----PDFIPSQPEGVFLYSKYR---
-
HUTH_HUMAN   LGLLDNEDRLEVALENNEFVEVVIEGDAMS-----PDFIPSQPEGVLYLSKYR---
-
HUTH_CAEL    NSLLDPEDLVSDVLKDSDFIIVAASVEETEDAKEAKKQEEIDNARAEIEKIDNRRRKVSF
HUTH_BACS    -----
-
HUTH_STRGR   -----
-
HUTH_CORY    -----
-

HUTH_PSEPU  -----
TELTLPKPGTLTLAQLRAIHAAPVRLQLDASAAPIDASVACVEQIIA
HUTH_RHIME  -----
MTVILRPGSVPLSDLETIYWTGAPARLDAAFDAGIAKAAARIAEIVA
HUTH_MOUSE  -----
EPEKYIALDGDLSLSTEDLVNLGKGGRYKIKLTSIAEKKVQQSREVIDSIK
HUTH_RAT     -----
EPEKYIALDGDLSLSTEDLVNLGKGGRYKIKLTSIAEKKVQQSREVIDSIK
HUTH_HUMAN   -----
EPEKYIELDGDRLTEDLVNLGKGGRYKIKLTPAEKRVQKSREVIDSIK
HUTH_CAEL    ADSLAPMVLAPPTKLLILDGNSLLPEDLVRCEKGECAIQLSMESEDRIRKARTFLEKIAS
HUTH_BACS    -----
MVTLDGSSLTTADVARVLFDFEEAAASEESMERVKKSRAAVERIVR
HUTH_STRGR   -----
MDMHTVVVGTS GTTAEDVVAVARHGARVELSAAAVEALAAARLIVDALAA
HUTH_CORY    -----
MASAPQITLGLSGATADDVIAVARHEARISISPOVLEELASVRAHIDALAS

```

Figure 13 cont'd.

HUTH_PSEPU
EDRTAYGINTGFGLLASTRIASHDLENLQ RSLVLSHAAGIGAPLDDDLVRLIMVLKINSL
HUTH_RHIME
GNAPVYGINTGFGKGLASIKIDSSDVATLQRNLILSHCCGVGQPLTEDIVRLIMALKLISL
HUTH_MOUSE
ERTVVYGITTGFGKFARTVIPANKLQELQVNLVRSHSSGVGKPLSPERCRMLLALRINVL
HUTH_RAT
ERTVVYGITTGFGKFARTVIPANKLQELQVNLVRSHSSGVGKPLSPERCRMLLALRINVL
HUTH_HUMAN
EKTVVYGITTGFGKFARTVIPINKLQELQVNLVRSHSSGVGKPLSPERCRMLLALRINVL
HUTH_CAEEL
EHRVYGVTTGFGTFSNVTIPPEKLKKLQNLIRSHATGYGEPLAPNRARMLLALRINIL
HUTH_BACS
DEKTIYGINTGFGKFSVDLIQKEDSAALQNLILSHACGVGDPFPECVSRAMLLLRANAL
HUTH_STRGR
KPEPVYGVSTGFGALASRHIGTELRAQLQRNIVRSHAAGMGRVEREVVRALMFLRLKTV
HUTH_CORY
ADTPVYGISTGFGALATRHIAPEDRAKLQRSLIRSHAAGMGEPVEREVVRALMFLRAKTL

HUTH_PSEPU
SRGFSGIRRKVIDALIALVNAEVYPHIPLKGSVGASGDLAPLATMSLVLLGEGKARYKGQ
HUTH_RHIME
GRGASGVRLELVRLIEAMLDKGVIPLIPEKGSVGASGDLAPLAHMAAVMMGHGEAFFAGE
HUTH_MOUSE
AKGYSGISLETCLKQVIEAFNASCLSYVPEKGTVGASGDLAPLSHLALGLIGEGKMWSPKS
HUTH_RAT
AKGYSGISLETCLKQVIEVFNASCLSYVPEKGTVGASGDLAPLSHLALGLIGEGKMWSPKS
HUTH_HUMAN
AKGYSGISLETCLKQVIEMFNASCLPYVPEKGTVGASGDLAPLSHLALGLVGEKGMWSPKS
HUTH_CAEEL
AKGHSGISVENIKKMIAAFNAFCVSYVPQQGTVGCSGDLCPALHLALGLLGEKGMWSPTT
HUTH_BACS
LKGFSGVRAELIEQLLAFLNKRVPVIPPQQGSLGASGDLAPLSHLALALIGQGEVFFEGE
HUTH_STRGR
ASGHTGVRPEVAQTMADV LNAGITPVVHEYGSLGCSGDLAPLSHCAL TLMGEGEAE GPDG
HUTH_CORY ASGRS-
VRPVVLETMVGM LNAGITPVVREY GSLGCSGDLAPLSHCALVLMGEGEATDAHG

HUTH_PSEPU -
WLSATEALAVAGLEPLTLAAKEGLALLNGTQASTAYALRGLFYAEDLYAAAACGGLSV
HUTH_RHIME -
RMKGDAALKAAGLSPVTLAAKEGLALINGTQVSTALALAGLFRAHRAGQAALITGALST
HUTH_MOUSE
GWADAKYVLEAHGLKPIVLKPKEGLALINGTQMITSLGCEALERASAIARQADIVAALT
HUTH_RAT
GWADAKYVLEAHGLKPIVLKPKEGLALINGTQMITSLGCEAVERASAIARQADIVAALT
HUTH_HUMAN
GWADAKYVLEAHGLKPIVLKPKEGLALINGTQMITSLGCEAVERASAIARQADIVAALT
HUTH_CAEEL
GWQPADVVLKKNLEPLELGPKEGLALINGTQMTALGAYTLERAHNIARQADVIAALS
HUTH_BACS -
RMPAMTGLKKAGIQPVTLSKEGLALINGTQAMTAMGVVAYIEAEKLAYQTERIASLTI
HUTH_STRGR
TVRPAGELLAAHGIAPVELREKEGLALLNGTDGMLGMLVMALADLRNLYTSADITAALS
HUTH_CORY
DIRPVPELFAEAGLTPVELAEKEGLALVNGTDGMLGQLIMALADLDELDDIADATAAMSV

Figure 13 cont'd.

HUTH_PSEPU EAVLGSRSPFDARIHE-ARGQRGQIDTAACFRDLLGDSSEVSLSHKNCD----
KVQDPYS
HUTH_RHIME DAAMGSSAPFHPDIQH-CAAIRARSTRAAALRQLLTG-SPIRQSHIEGDE---
RVQDPYC
HUTH_MOUSE EVLKGTTKAFDTDIHA-VRPHRGQIEVAFRFRSLLDS-
DHHPSEIAESHRFCDRVQDAYT
HUTH_RAT EVLKGTTKAFDTDIHA-VRPHRGQIEVAFRFRSLLDS-
DHHPSEIAESHRFCDRVQDAYT
HUTH_HUMAN EVLKGTTKAFDTDIHA-LRPHRGQIEVAFRFRSLLDS-
DHHPSEIAESHRFCDRVQDAYT
HUTH_CAEEL DVLKGTTTRAYDPDIHR-IRPHRGQNL SALRLRALLHS-
EANPSQIAESHRNCTKVQDAYT
HUTH_BACS EGLQGIIDAFDEDIHL-ARGYQE QIDVAERIRFYLS- SGLTTSQGE-----
LRVQDAYS
HUTH_STRGR EALLGTDKVLAPELHA-IRPHPGQGV SADNMSRVLAG- SGLTGHHQDDAP---
RVQDAYS
HUTH_CORY EAQLGTDQVFRAELHEPLRPHPGQGRSAQNMFAFLAD-SPIVASHREGDG---
RVQDAYS

HUTH_PSEPU
LRCQPQVMGACLTQLRQAAEVLGIEANAVSDNPLVFAAEGDVISGGNFHAEFPVAMAADNL
HUTH_RHIME IRCQPQVDGACLDLLRSVAATLTIEANAVTDNPLVLSDN-
SVVSGGNFHAEPVAFADQI
HUTH_MOUSE
LRCCPQVHGVVNDTIAFVKDIITTELNSATDNPMVFASRGETISGGNFHGEYPAKALDYL
HUTH_RAT
LRCCPQVHGVVNDTIAFVKDIITTELNSATDNPMVFASRGETISGGNFHGEYPAKALDYL
HUTH_HUMAN
LRCCPQVHGVVNDTIAFVKNIITTELNSATDNPMVFANRGETVSGGNFHGEYPAKALDYL
HUTH_CAEEL
LRCVPQVHGVVHDTIEFVREIITTEMNSATDNPLVFADREEIISGGNFHGEYPAKALDFL
HUTH_BACS
LRCIPQVHGATWQTLGYVKEKLEIEMNAATDNPLIFNDGDKVISGGNFHGQPIAFAMDFL
HUTH_STRGR VRCAPQVNGAGRDTLDHAALVAGRELASSVDNPVLPDG-
RVESNGNFHGAPVAYVLDLFL
HUTH_CORY LRCSPQVTGAARDTIAHARLVATRELA A AIDNPVLP SG-
EVTSNGNFHGAPVAYVLDLFL

HUTH_PSEPU ALAIAEIGSLSERRISLMDKHMS-
QLPPFLVENGGVNSGFMIAQVTAALASENKALSH
HUTH_RHIME
ALAVCEIGAISQRRIALLVDPALSLRLPAFLAKKPGLNSGLMIAEVTSAALMSENKQLSH
HUTH_MOUSE AIGVHELAAISERRIERLCNPSLS-
ELPAFLVAEGGLNSGFMIAHCTAAALVSESKALCH
HUTH_RAT AIGVHELAAISERRIERLCNPSLS-
ELPAFLVAEGGLNSGFMIAHCTAAALVSESKALCH
HUTH_HUMAN AIGIHELAAISERRIERLCNPSLS-
ELPAFLVAEGGLNSGFMIAHCTAAALVSENKALCH
HUTH_CAEEL AIAVAELAQMSERRERLERNKELS-
GLPTFLTPDGGLNSGFM TVQLCAASLVSENKVLCH
HUTH_BACS KIAISELANIAERRIERLVNPQLN-
DLPPFLSPHPGLQSGAMIMQYAAASLVSENKTLAH
HUTH_STRGR
AIVAADLGSICERRTDRLLDKNRSHGLPPFLADDAGVDSGLMIAQYTQAALVSEMKRLAV
HUTH_CORY
AIAVADLGSIAERRTDRMLDPAERSDLPAFLADDPGVDSGMMIAQYTQAGLVAENKRLAV

Figure 13 cont'd.

HUTH_PSEPU	PHSVDSLPTSANQEDHVSMAAAGKRLWEMAENTRGVPAIEWLGACQGLDLRKG-LKTS
HUTH_RHIME	PASVDSTPTSANQEDHVSMAHGARRLLQMTENLFSIIGIEALAAVQGIEFRAP-LTTS
HUTH_MOUSE	PSSVDSLSTSAATEDHVSMMGGWAARKALRVVEHVEQVLAIELLAACQGIEFLRP-LKTT
HUTH_RAT	PSSVDSLSTSAATEDHVSMMGGWAARKALRVIEHVEQVLAIELLAACQGIEFLRP-LKTT
HUTH_HUMAN	PSSVDSLSTSAATEDHVSMMGGWAARKALRVIEHVEQVLAIELLAACQGIEFLRP-LKTT
HUTH_CAEEL	PSSVDSIPTSCNQEDHVSMMGGWAARKALTVVEHVEAVLAMELLAACQGIEFLKP-LIST
HUTH_BACS	PASVDSIPSSANQEDHVSMTIARHAYQVIANTRRVIAIEAICALQAVEYRGI-EHAA
HUTH_STRGR	
PASADSIPSSAMQEDHVSMMGWSAARKLRATAVDNLARIVAVELYAATRAIELRAAEGLTPA	
HUTH_CORY	PA-VDSIPSSAMQEDHVS LGWHAARKLPTSVANLRRILAVEMLIAGRALDLRAP-LKPG
HUTH_PSEPU	AKLEKARQALRSEVA-HYDRDRFFAPDIEKAVELLAAG---S-LTGLLPAGVLPPL---
HUTH_RHIME	PELQKAAAARGVSS-SIEEDRYMADDLKAAGDLVASG---R-LAAAVSAGILPKLEN---
HUTH_MOUSE	TPLEKVYDLVRSVVR-
PWIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEKYRMEHIPESR	
HUTH_RAT	TPLEKVYDLVRSVVR-
PWIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEKYRMEHIPESR	
HUTH_HUMAN	TPLEKVYDLVRSVVR-
PWIKDRFMAPDIEAAHRLLEQKVWEVAAPYIEKYRMEHIPESR	
HUTH_CAEEL	APLHKIYQLVRSVAP-
PLNEDRYMKPEIDAVLEMIRENRIWEAVLPHLETLEAMEELDPD	
HUTH_BACS	SYTKQLFQEMRKVVP-SIQQDRVFSYDIERLTDWLKK---ESLIPDHQNKELRGMNI---
HUTH_STRGR	PASEAVVAALRAAGAEGPGPDRFLAPDLAAADTFVREG---R-LVAAVEPVTGPLA---
HUTH_CORY	PATGAVLEVLRSKVA-GPGQDRFLSAELEAAAYDLLANG---S-VHKALEAHLPE-----
HUTH_PSEPU	-----
HUTH_RHIME	-----
HUTH_MOUSE	PLSPTAFSLES LRKNSATIPESDDL----
HUTH_RAT	PLSPTAFSLES LRKNSATIPESDDL----
HUTH_HUMAN	PLSPTAFSLQFLHKKSTKIPESDDL----
HUTH_CAEEL	ALRQFTKTPTGIVQDRSMIPISDDEESIE
HUTH_BACS	-----
HUTH_STRGR	-----
HUTH_CORY	-----

Figure 14

	983831	1	80
1	SWALL: CAC21618	100.0%	MASAPQITGLSGATADDVIAVARHEARISISPOVLEEELASVRAHIDALASADTPVYGI STGFGALATRHIAPEDRAKLQ
2	SWALL: HUTH_STRGR	66.1%	---MHTVVVGTSVGTASDVLAVARAGARIELSEEAVALAAARSVDALAAPDPVYGVYSTGFGALATRHISPRLGRQLQ
3	SWALL: HUTH_DEIRA	65.4%	---MDMHTVVVGTSVGTAEADVVARHGHARVELSAAVEALAAARLIVDALAAKPEPVPYGVYSTGFGALASRHIGTELRAQLQ
4	SWALL: BAB16159	46.8%	-----MILDRDLNLEQFTSVVRHGHQVELSAAARERARARTVIEQIVEGDTPIYGVNTGFGFENVQIDRSQLAQLQ
5	SWALL: Q9KWE4	42.0%	-----VPLHHIADIYWNNGSAKLDPSFDAAVLKGAARAEIAAGNAPVYGIN TGFGKLASIKIDAADLALTLQ
6	SWALL: HUTH_BACSU	42.0%	-----VPLHHIADIYWNNGSAKLDPSFDAAVLKGAARAEIAAGNAPVYGIN TGFGKLASIKIDAADLALTLQ
7	SWALL: Q9KSQ4	40.4%	---MVTLDGSSLTADVARVLFDFEEAAASESMERVKKSRAAVERIVRDEKTIYGIN TGFGKESDVLIOKEDSAAQLQ
8	SWALL: Q9HU85	42.2%	---MLHLMIKPGQSLKQLRQVSRSPVVLSDPEAIPATAESAQVVEQVISEGRTVYGIN TGFGLIANTKIAIPQDLETLQ
9	SWALL: Q9KBE6	41.7%	---MSHLKPGQITLADLRQAYLAPVRLSLDPSADAPTAAASVACVENIIAEGRTAYGIN TGFGLLASTRISPADLEKLQ
10	SWALL: HUTH_PSEPU	39.3%	---MTNLKLLDGRSLSLHDLHRIIYEGETV GASDESMEKVQKSRKAVEQIIVADEKIIYGI TTGFGKESDIFIDPDDVLENLQ
11	SWALL: HUTH_RHIME	41.7%	---TELTKPGTITLAQRAIHAAPVRLQDASAPADASVACVEQIIAEDRTAYGIN TGFGLIASTRIASHDLENLQ
12	SWALL: Q9HU90	40.6%	-----LRPGSVPLSDLETIYWTGAPARLDAADFAGTAKAARAEIAAGNAPVYGIN TGFGKLASIKIDSSDVATILQ
13	SWALL: HUTH_HUMAN	40.7%	MSDLP SVVFGDGPLRWQELVAVARHGARLELSAAAWARIDNARAIVCRIVANGERAYGI STGLGALCDVLLEGEQLAELS
14	SWALL: HUTH_CAEEL	39.2%	KYREPEKYIELDGLTTEDLVNLGKGRYKIKLTPTAEKRVQKSREVIDSIIKEKTVVYGI TTGFGKFA-RTVIPINKLQILQ
15	SWALL: Q9HLI6	38.8%	VLAPPTKLLILDGNSPEDLVRCCEKGECAIQLSMESEDRIRKARTFLEKIASEHRAVYGV TTGFTFSNVTIPPEKLLKILQ
16	SWALL: HUTH_MOUSE	41.0%	---MTEIDGRSILRVEDVYAVAYEYDRVSI SDTILKAVEEKHEAFKLINSKTVYGV NTGFGSLLNHIERDQETELQ
17	SWALL: BAB29407	38.6%	KYREPEKYIALDGDSTEDLVNLGKGRYKIKLTSIAEKKVQQSREVIDSIIKERTVVYGI TTGFGKFA-RTVIPANKLQILQ
18	SWALL: HUTH_RAT	38.2%	KYREPEKYIALDGDSTEDLVNLGKGRYKIKLTSIAEKKVQQSREVIDSIIKERTVVYGI TTGFGKFA-RTVIPANKLQILQ
19	SWALL: AAG53586	39.8%	KYREPEKYIALDGDSTEDLVNLGKGRYKIKLTSIAEKKVQQSREVIDSIIKERTVVYGI TTGFGKFA-RTVIPANKLQILQ
20	SWALL: Q9KKE0	38.9%	---MNAULTLTPTGLTTLAQRFQVWQQLTLDESAAHEAINDSVACVEAIVAEGR TAYGIN TGFGLLAQTRTATHDLENLQ
21	SWALL: Q9HQD5	42.2%	-----MGEMISLDGPLTWREIASIAEGASLDLSGPARURIAQARRIVDALVERGIRGYGIN TGVGALCDVTISRENQQOALS
			-----MSDTRIDAADREALQ

Figure 14, cont'd.

	983831	81	1	160
1	SWALL: CAC21618	100.0%	RSLSRSHAAGMGEPREREVRALMFLRAKTLASRTGTGRPVVLETWGMNAGTTPVVREYSGSLGSGDLAPLSHCALVL	
2	SWALL: HUTH_STRGR	66.1%	RNIVRSHAAGMGEPREREVRALMFLRAKTLASRTGTGRPVVLETWGMNAGTTPVVREYSGSLGSGDLAPLSHCALVL	
3	SWALL: HUTH_DEIRA	65.4%	RNIVRSHAAGMGEPREREVRALMFLRAKTLASRTGTGRPVVLETWGMNAGTTPVVREYSGSLGSGDLAPLSHCALVL	
4	SWALL: BAB16159	46.8%	HNLIIVSHAIGMGEPLAEVVRGMLLRQAQSLSGHSGVRVEVVELLIALINADALPVVPSQGSVGSGDLAPLAHLALGL	
5	SWALL: Q9KWE4	42.0%	RNLIILSHCCGVGAPLPENVRVRLIMALKLISLGRGASGVRIELIRLIEGMLEKGVIPVPIPEKGSVGSGDLAPLAHMSATM	
6	SWALL: HUTH_BACSU	42.0%	RNLIILSHCCGVGAPLPENVRVRLIMALKLISLGRGASGVRIELIRLIEGMLEKGVIPVPIPEKGSVGSGDLAPLAHMSATM	
7	SWALL: Q9KSQ4	40.4%	LNLIILSHACGVGDPPFECVSRAMLLLRANALLKGFSGVRAELIEQLAFLNKRHPVPIPOQGSVGSGDLAPLSHLALAL	
8	SWALL: Q9HU85	42.2%	KSIVLSHAAGVGEALDDAMVRLVMLLKMINSIARGYSGIRLEVIQALIELVNNQIYPCVPKKGSGSGDLAPLAHMSATM	
9	SWALL: Q9KBE6	41.7%	RSIVLSHAAGVGEALDDAMVRLVMLLKMINSIARGYSGIRLEVIQALIELVNNQIYPCVPKKGSGSGDLAPLAHMSATM	
10	SWALL: HUTH_PSEPU	39.3%	HNLIYSHACGVGSPFETVSRMTMLVRANALLKGFSGVRPLVIERLIALVNANIHPIVPOQGSVGSGDLAPLSHLALVL	
11	SWALL: HUTH_RHIME	41.7%	RSIVLSHAAGVGEALDDAMVRLVMLLKMINSIARGYSGIRLEVIQALIELVNNQIYPCVPKKGSGSGDLAPLAHMSATM	
12	SWALL: Q9HU90	40.6%	RNLIILSHCCGVGQPLTEDIVRLIMALKLISLGRGASGVRIELVRLIEAMLDKGVIPVPIPEKGSVGSGDLAPLAHMAAVM	
13	SWALL: HUTH_HUMAN	40.7%	RNLIILSHCCGVGQPLTEDIVRLIMALKLISLGRGASGVRIELVRLIEAMLDKGVIPVPIPEKGSVGSGDLAPLAHMAAVM	
14	SWALL: HUTH_CAEEL	39.2%	RNLIILSHCCGVGQPLTEDIVRLIMALKLISLGRGASGVRIELVRLIEAMLDKGVIPVPIPEKGSVGSGDLAPLAHMAAVM	
15	SWALL: Q9HLLT6	38.8%	LNLIIRSHATGYGEPLAPNARMILLALRINILAKGHSIGSVENIKKMTAAFNATCVSYVPOQGTVCSCGDLAPLSHLALGL	
16	SWALL: HUTH_MOUSE	41.0%	KNLIIRSHSSGVGDYLENRYVRAMVAINSLAAGYSVADLLNMVEMLNIRDVIPAIPKYGSGSGDLAPLAHIGLAM	
17	SWALL: BAB29407	38.6%	VNLIIRSHSSGVGDYLENRYVRAMVAINSLAAGYSVADLLNMVEMLNIRDVIPAIPKYGSGSGDLAPLAHIGLAM	
18	SWALL: HUTH_RAT	38.6%	VNLIIRSHSSGVGDYLENRYVRAMVAINSLAAGYSVADLLNMVEMLNIRDVIPAIPKYGSGSGDLAPLAHIGLAM	
19	SWALL: AAG53586	38.2%	VNLIIRSHSSGVGDYLENRYVRAMVAINSLAAGYSVADLLNMVEMLNIRDVIPAIPKYGSGSGDLAPLAHIGLAM	
20	SWALL: Q9KKE0	39.8%	RSIVLSHAAGVGEPLDDDIVRLMMVLKINSIARGFSGIRLSVIOALIALVNAGVYSVDPKAGSGSGDLAPLAHMSITL	
21	SWALL: Q9HQD5	38.9%	RNLIILSHACGVGDPLGRVEARAVMAAQIANLTHCYSGVRVETAEMLLIALINADIIPVPSRGSVGSGDLAPLAHMSITL	
		42.2%	ANLIIRSHAAGAGSELDTAAVRALLVTRINALAKYSGIRERVRDLVGLLNEGVRHVPVPSRGSVGSGDLAPLAHMSRVL	

Figure 14, cont'd.

	983831	161	240
1	SWALL: CAC21618	100.0%	MGEGEATDAGHDIRPVPELFABEAGLTPVELAEKEGLALVNGTGMGLGQIMALADLDELIDADIADATAMSVAEQIGTQDV
2	SWALL: HUTH_STRGR	66.1%	MGEGDAEGPDGTVRAGELLAAHGIAPIVELREKEGLALINGTGMGLMVLMAADLDTLYKSADITPAALTMELLLGTDRV
3	SWALL: HUTH_DEIRA	65.4%	MGEGEAEGPDGTVRAGELLAAHGIAPIVELREKEGLALINGTGMGLMVLMAADLRLNLYTSADITPAALTMELLLGTDRV
4	SWALL: BAB16159	46.8%	IGLGD1-EYQGVQVPAADVLAEGLSPVQLOAKEGLALINGTGMGLMVLMAADLRLNLYTSADITPAALTMELLLGTDRV
5	SWALL: Q9KWE4	42.0%	MGEGEAF-YQGVQVPSKDALAKAGLSPVLAKEGLALINGTGMGLMVLMAADLRLNLYTSADITPAALTMELLLGTDRV
6	SWALL: HUTH_BACSU	42.0%	MGEGEAF-YQGVQVPSKDALAKAGLSPVLAKEGLALINGTGMGLMVLMAADLRLNLYTSADITPAALTMELLLGTDRV
7	SWALL: Q9KSQ4	40.4%	IGQGEVF-FEGERPAMTGLKKAGIQPVTLTSKEGLALINGTGMGLMVLMAADLRLNLYTSADITPAALTMELLLGTDRV
8	SWALL: Q9HU85	42.2%	LGEQAR-YNGKIIISGLEAMKTAGLEPTLPAKEGLALINGTGMGLMVLMAADLRLNLYTSADITPAALTMELLLGTDRV
9	SWALL: Q9KBE6	41.7%	IGESRARH-RGEWLPAAEALAVAGLEPTLPAKEGLALINGTGMGLMVLMAADLRLNLYTSADITPAALTMELLLGTDRV
10	SWALL: HUTH_PSEPU	39.3%	LGEQAR-YNGKIIISGLEAMKTAGLEPTLPAKEGLALINGTGMGLMVLMAADLRLNLYTSADITPAALTMELLLGTDRV
11	SWALL: HUTH_RHIME	41.7%	LGEQAR-YNGKIIISGLEAMKTAGLEPTLPAKEGLALINGTGMGLMVLMAADLRLNLYTSADITPAALTMELLLGTDRV
12	SWALL: Q9HU90	40.6%	MGEGEAF-YQGVQVPSKDALAKAGLSPVLAKEGLALINGTGMGLMVLMAADLRLNLYTSADITPAALTMELLLGTDRV
13	SWALL: HUTH_HUMAN	40.7%	LGIGEVF-YKGTWKASFALEKEEIEPTLTAKEGLALINGTGMGLMVLMAADLRLNLYTSADITPAALTMELLLGTDRV
14	SWALL: HUTH_CAEEL	39.2%	MGEGEAF-YQGVQVPSKDALAKAGLSPVLAKEGLALINGTGMGLMVLMAADLRLNLYTSADITPAALTMELLLGTDRV
15	SWALL: Q9HLLT6	38.8%	LGIGEVF-YKGTWKASFALEKEEIEPTLTAKEGLALINGTGMGLMVLMAADLRLNLYTSADITPAALTMELLLGTDRV
16	SWALL: HUTH_MOUSE	41.0%	MGEGEAF-YQGVQVPSKDALAKAGLSPVLAKEGLALINGTGMGLMVLMAADLRLNLYTSADITPAALTMELLLGTDRV
17	SWALL: BAB29407	38.6%	LGIGEVF-YKGTWKASFALEKEEIEPTLTAKEGLALINGTGMGLMVLMAADLRLNLYTSADITPAALTMELLLGTDRV
18	SWALL: HUTH_RAT	38.2%	MGEGEAF-YQGVQVPSKDALAKAGLSPVLAKEGLALINGTGMGLMVLMAADLRLNLYTSADITPAALTMELLLGTDRV
19	SWALL: AAG33586	39.8%	LGIGEVF-YKGTWKASFALEKEEIEPTLTAKEGLALINGTGMGLMVLMAADLRLNLYTSADITPAALTMELLLGTDRV
20	SWALL: Q9RKE0	38.9%	IGHGSAMQGTERTLSGADAL-ARLGLAPLRLEAKESLIVNGTGMGLMVLMAADLRLNLYTSADITPAALTMELLLGTDRV
21	SWALL: Q9HQD5	42.2%	IGEGQA-DVAGERMPAAEALAAADLEPVTLQAKEGLALINGTGMGLMVLMAADLRLNLYTSADITPAALTMELLLGTDRV

Figure 14, cont'd.

	983831	241	320
1	SWALL: CAC21618	100.0%	IRAEELHPIRPHPGGRSAQNMFADLSPVIVASHREGDRVQDAYSLRCSQVGTGAARDTIAHARLVATRELAAAI
2	SWALL: HUTH_STRGR	66.1%	IAPELHA-IRPHPGQAASAAANMAAVLKSGSLTGHQDDAPRVQDAYSVRCAPVAGAGRTMAHAGLVAERELAAAVDNP
3	SWALL: HUTH_DEIRA	65.4%	IAPELHA-IRPHPGQGVSAONMSRVLAGSLTGHQDDAPRVQDAYSVRCAPVAGAGRTLDHAALVAGRELASSVDNP
4	SWALL: BAB16159	46.8%	FQPDV-VGLRPHPGALAAELREFLAGSEIAFSLHTGDKVQDAYSLRAVPQVHGATWADALAAERVLAVEFASVTDNP
5	SWALL: Q9KWE4	42.0%	FHPDIHT-LRGHKQIDAGSALRNLLQSGEIRFESHIEGDERVQDPYCIRCPQVDGACLDLLASVARTLEIANAVTDNP
6	SWALL: HUTH_BACSU	42.0%	FHPDIHT-LRGHKQIDAGSALRNLLQSGEIRFESHIEGDERVQDPYCIRCPQVDGACLDLLASVARTLEIANAVTDNP
7	SWALL: Q9KSQ4	40.4%	FDEDIHLA-RGYQEQIDVAERIRFYLSDSGLTTS--QGEIRVQDAYSLRCPQVMGACIQQIRSAEVLVEANVSVDNP
8	SWALL: Q9HU85	42.2%	FDPRIHR-VRGHRQMDAATAYRHLLVSSIEIGQSHSNC--KVQDPYSLRCPQVMGACLTQMRQAEVLVEANVSVDNP
9	SWALL: Q9KBE6	41.7%	FDARIHA-RGQRQIDVAAAYRDLLASSEVARSHKCD--KVQDPYSLRCPQVMGACLTQMRQAEVLVEANVSVDNP
10	SWALL: HUTH_PSEPU	39.3%	FDEQIHEA-RGYVEQDVARMESYLDSSQLT--RQGEIRVQDAYSLRCPQVMGACLTQMRQAEVLVEANVSVDNP
11	SWALL: HUTH_RHIME	41.7%	FDARIHEA-RGQRQIDTAACFRDLIGDSSEYSSHKNC--KVQDPYSLRCPQVMGACLTQMRQAEVLVEANVSVDNP
12	SWALL: Q9HU90	40.6%	FHPDIQCAAIRARSTRAAA-LRQLTGSPIRQSHIEGDERVQDPYCIRCPQVDGACLDLLASVARTLEIANAVTDNP
13	SWALL: HUTH_HUMAN	40.7%	FDAEI-VALKPHPGMQRVAANLRALLAGSQVLENAR--GIRTQDALSIQIHGACRDLAHARQIET-ELNSATDNP
14	SWALL: HUTH_CAEEL	39.2%	FDTDIHA-LRPHRGQIEVAFRFRSLSDSEIAESHRFCD--RVQDAYTLRCCPQVHGAVNDTIAFKNIIITTELSATDNP
15	SWALL: Q9HLI6	38.8%	YDPDIHR-IRPHRGQNLALRLALINPSQIAESHRNCT--KVQDAYTLRCCPQVHGAVNDTIAFKNIIITTELSATDNP
16	SWALL: HUTH_MOUSE	41.0%	FTPWILGA-RPHLGQVAIGNRFREYLTGSDIV--KRADSVKQDAYTLRCPQVYGSVADVIDVENVLSVEINSATDNP
17	SWALL: BAB29407	38.6%	FDTDIHA-VRPHRGQIEVAFRFRSLSDSEIAESHRFCD--RVQDAYTLRCCPQVHGAVNDTIAFKNIIITTELSATDNP
18	SWALL: HUTH_RAT	38.6%	FDTDIHA-VRPHRGQIEVAFRFRSLSDSEIAESHRFCD--RVQDAYTLRCCPQVHGAVNDTIAFKNIIITTELSATDNP
19	SWALL: AAG53586	38.2%	FDTDIHA-VRPHRGQIEVAFRFRSLSDSEIAESHRFCD--RVQDAYTLRCCPQVHGAVNDTIAFKNIIITTELSATDNP
20	SWALL: Q9KKE0	39.8%	FAELPLALRQSGLSAVGEGRLDWLADSPMLAG--TAGTRTQDPLSLRAVPQVHGAGARDAFGQVAEIVDRELASVTDNP
21	SWALL: Q9HQD5	38.9%	CAPAIHE-VRPHDGQAVSARHIRNLTAGSEVLDDHHRDCD--RVQDAYSIKRLCPQVHGAVRDALDHLRAAVATELSATDNP
		42.2%	

Figure 14

Figure 14, cont'd.

	321	400
983831	100.0%	
1 SWALL: CAC21618	66.1%	VVLPDGRVESNGNFHGPVAVYVLD
2 SWALL: HUTH_STRGR	65.4%	VVLPDGRVESNGNFHGPVAVYVLD
3 SWALL: HUTH_DEIRA	46.8%	LIIFTGEVVSNGNFHGPVAVYVLD
4 SWALL: BAB16159	42.0%	LVLSDNSVVSNGNFHGPVAVYVLD
5 SWALL: Q9KWE4	42.0%	LVLSDNSVVSNGNFHGPVAVYVLD
6 SWALL: HUTH_BACSU	40.4%	LIENDGDVVSNGNFHGPVAVYVLD
7 SWALL: Q9KSQ4	42.2%	LVFADGDVVSNGNFHGPVAVYVLD
8 SWALL: Q9HU85	41.7%	LVFAAGDVVSNGNFHGPVAVYVLD
9 SWALL: Q9KBE6	39.3%	LIENDGDVVSNGNFHGPVAVYVLD
10 SWALL: HUTH_PSEPU	41.7%	LVFAAGDVVSNGNFHGPVAVYVLD
11 SWALL: HUTH_RHIME	40.6%	LVFAAGDVVSNGNFHGPVAVYVLD
12 SWALL: Q9HU90	40.7%	LLGTPVVSQANPHGESVMAADNLAIAE
13 SWALL: HUTH_HUMAN	39.2%	LVFANGETVVSNGNFHGPVAVYVLD
14 SWALL: HUTH_CAEEL	38.8%	LVFADREIISGGNFHGPVAVYVLD
15 SWALL: Q9HLI6	41.0%	L-FNGEEVVSNGNFHGPVAVYVLD
16 SWALL: HUTH_MOUSE	38.6%	MVFASGETISGGNFHGPVAVYVLD
17 SWALL: BAB29407	38.6%	MVFASGETISGGNFHGPVAVYVLD
18 SWALL: HUTH_RAT	38.2%	MVFASGETISGGNFHGPVAVYVLD
19 SWALL: AAG53586	39.8%	LVFAANEMVFRGNFHAEPVMAADNLAIAE
20 SWALL: Q9KKE0	38.9%	AVAGSPEVHSQAHAVGAALGLAMD
21 SWALL: Q9HQD5	42.2%	LVFPSTVVSNGNFHGPVAVYVLD

[illegible]

Figure 14, cont'd.

	983831	481	[.	5	.] 513
1	SWALL: CAC21618	100.0%	PGQDRFLSAELEAAVDLLANGSVHKALEAHLPA				
2	SWALL: HUTH_STRGR	66.1%	PGPDRHLAPDLAAADAFVRAGHLVAAAESVTGP				
3	SWALL: HUTH_DEIRA	65.4%	PGPDRFLAPDLAAADTFVREGRLVAAVEPTGP				
4	SWALL: BAB16159	46.8%	LTEDRYFRPDLRLRGELVSGRVAQAADTQAPA				
5	SWALL: Q9KWE4	42.0%	IEDDRYMATDLKAAIEVVASGALVSAISSGLPV				
6	SWALL: HUTH_BACSU	42.0%	IEDDRYMATDLKAAIEVVASGALVSAISSGLPV				
7	SWALL: Q9KSQ4	40.4%	IQQDRVFSYDIERLTDWLKESLIPDHQNKELR				
8	SWALL: Q9HU85	42.2%	YKDRYFAPDIEKANALL-QLAVHNRIMPDQLL				
9	SWALL: Q9KBE6	41.7%	YQEDRFFAPDIEAASQILLASGCINALLPARLLP				
10	SWALL: HUTH_PSEPU	39.3%	IDQDRMFAKDI ERAAKWLKDGSDFTKMKREKER				
11	SWALL: HUTH_RHIME	41.7%	YDRDRFFAPDIEKAVELLAKGSLTGLLPAGLPS				
12	SWALL: Q9HU90	40.6%	TEEDRYMADLKAAGDLVASGRLAASVAGLPGK				
13	SWALL: HUTH_HUMAN	40.7%	YDTRWLAPDIAASAAAILGERKSLARLAASIGD				
14	SWALL: HUTH_CAEEL	39.2%	WIKDRFMAPDIEAAHRLLEOKVWEVAAPYIEK				
15	SWALL: Q9HLI6	38.8%	PNEDRYMKPEIDAVLEMIRENRIWEAVLPHLET				
16	SWALL: HUTH_MOUSE	41.0%	LDHDRPSPFDIETIRKMMDRKEFISALP----				
17	SWALL: BAB29407	38.6%	WIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEK				
18	SWALL: HUTH_RAT	38.6%	WIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEK				
19	SWALL: AAG53586	38.2%	WIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEK				
20	SWALL: Q9KKE0	39.8%	YDDDRFFAPDIEAAISLLNKGSLVGLLPAFL--				
21	SWALL: Q9HQD5	38.9%	PIATIVR-----				
		42.2%	PAGDRALADDMAAVGDLVRAGLVEDAVARALDA				

Figure 14, cont'd.

KEY:

983831 : HAL

1 CAC21618 : Streptomyces coelicolor

2 HUTH_STRGR : Streptomyces griseus

3 HUTH_DEIRA : Deinococcus radiodurans

4 BAB16159 : Agrobacterium rhizogenes

5 Q9KWE4 : Agrobacterium rhizogenes

6 HUTH_BACSU : Bacillus subtilis

7 Q9KSQ4 : Vibrio cholerae

8 Q9HU85 : Pseudomonas aeruginosa

9 Q9KBE6 : Bacillus halodurans

10 HUTH_PSEPU : Pseudomonas putida

11 HUTH_RHIME : Rhizobium meliloti

12 Q9HU90 : Pseudomonas aeruginosa

13 HUTH_HUMAN : Human

14 HUTH_CAEEL : Caenorhabditis elegans

15 Q9HLI6 : Thermoplasma acidophilum

16 HUTH_MOUSE : Mouse

17 BAB29407 : Mus musculus (Mouse)

18 HUTH_RAT : Rat

18 AAG53586 : uncultured bacterium pCosAS1

20 Q9KKE0 : Rhizobium meliloti

21 Q9HQD5 : Halobacterium sp

STRG	6	VVGTSGTTAEDVVAVARHGARVELSAAAVEALAAARLIVDALAAKPEPVYGVSTGF
"HAL"	7	ITLGLSGATADDVIAVARHEARISISPQVLFEELASVRAHIDALASADTPVYGISTGF
		* * * * *
STRG,	66	ASRHIGTELRAQLQRNIVRSHAAAGMPRVEREVVRALMFLRLKTVASGHTGVRPEVAQT
HAL	67	ATRIAPEDRAKLQRSIRSHAAAGMGEPEVEREVVRALMFLRAKTLASGRTGVRPVL
		* * * * *
		* * * * *
STRG	126	ADVLNAGITPVVHEYGSLGCSGDLAPLSHCALTLMGEAECPDGTVPAGELLA
HAL	127	VGMLNAGITPVVREYGS LGCSGDLAPLSHCALVLMGEAEATDAHGDIRPPELF
		* * * * *
		* * * * *
STRG	186	PVELREKEGLALLNGTDGMLVMALADLRNLTSADITAALSLEALLGTDKVL
HAL	187	PVELAEKEGLALVNGTDGMLGQLIMALADLDELLDIADATAAMSVEAQLGTDQVF
		* * * * *
		* * * * *
STRG	246	A-IRPHPGQVSADNMRSVLAGSGLTGHHQDDAPRVQDAYSVRCAPQVNGAGRDTLD
HAL	247	EPLRHPGQGRSAQNMFALADSPIVASHREGDGRVQDAYSLRCSPPQVTGAARDT
		* * * * *
		* * * * *
STRG	305	LVAGRELASSVDNPVLPDGRVESNGNFHGAPVAYVLDFLAIVAADLGSIERRTR
HAL	307	LVATR ELAAAIDNPVLPSPGEVTSNGNFHGAPVAYVLDFLAIAVADLGSIERRTR
		* * * * *
		* * * * *

Figure 15, Cont'd.

STRG	365	KNRSHGLPPFLADDAGVDSGLMIAQYTQAALVSEMKRLAVPASADSI PSSAMQEDHVS MG
HAL	367	PARSRDLP AFLADDPGVDSGMMIAQYTQAGLVAENKRLAVPASVDSI PSSAMQEDHVS LG
		** ** *
STRG	425	WSAARKLRTAVDNLARI VAVELYAA TRAI ELRAA EGLTPAPASEAVVAALRAAGAE GPGP
HAL	427	WHAARKLRTSVANLRRILAVEMLIAGRALDLRAP--LKPGPATGAVLEVLRSKVA-GPGQ
		* *
STRG	485	DRFLAPDLAAADTFVREGRLVA AVE
HAL	484	DRFLSAELEAA YDLLANGSVHKALE
		*** * * * *